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Bacterial diversity characterization of naturally radioactive mineral springs: Role of these bacterial communities in uranium biogeochemistry

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Microorganisms are the first living beings to have appeared on Earth, and populate many habitats, including the most extreme. Among these environments, some are characterized by naturally high levels of radiation where microorganisms have developed over thousands of years by adopting various strategies to respond to the stresses induced by ionizing radiation [1]. Naturally radioactive mineral springs are therefore ecosystems where ionizing radiation could constitute an abiotic driver impacting the diversity and structure of microbial communities.

The primary objective of the TIRAMISU collaboration, within the “Zone Atelier Territoires Uranifères (ZATU)”, is to understand the effects of radioelements (radiation / chemical toxicity) on microbial communities from a diverse range of naturally radioactive mineral springs in the French Massif Central (Auvergne). The Massif Central is a region made up of uranium-rich geological formations (granite massif), well known for its naturally radioactive mineral sources. Microbial inhabitants of natural uranium enriched environment exhibit various adaptive features to support their growth and survival, giving rise to uranium tolerant populations in such sites [2]. The objective of our study is to identify and characterize the bacterial communities in these mineral sources, and to understand their role in uranium biogeochemistry.

In this study, we focused on the study of samples from six naturally radioactive mineral springs of varying radioelement concentration gradient (<3.71 ppb U) in the Massif Central sampled in autumn and spring. The bacterial biodiversity of these samples was characterized by next generation sequencing (Illumina Miseq), targeting the 16S rRNA gene. In addition, the influence of the different physico-chemical parameters of these sources on these bacterial communities was studied. On a second hand, culturing on non-selective medium (TSB) was performed for samples from these six mineral springs and a seventh with a higher concentration of uranium (15.91 ppb U). A collection of 625 aerobically cultivable bacterial isolates, corresponding to 295 OTUs, was thus constituted via Sanger sequencing of the 16S rRNA gene. Subsequently, close relatives to known radiotolerant species were screened in uranium resistance experiments. The most resistant strains were further selected and characterized genetically and metabolically to understand the mechanisms behind their tolerance towards radioelements. These preliminary results will be discussed in the context of understanding the evolution, functionality and survival of microbial communities and their interactions with uranium in naturally radioactive sources.

[1]: Shuryak, Igor. « Review of Microbial Resistance to Chronic Ionizing Radiation Exposure under Environmental Conditions ». *Journal of Environmental Radioactivity* 196 (janvier 2019): 50-63

[2]: Chandwadkar, Pallavi, Hari Sharan Misra, and Celin Acharya. « Uranium Biomineralization Induced by a Metal Tolerant *Serratia* Strain under Acid, Alkaline and Irradiated Conditions ». *Metallomics* 10, no 8 (2018): 1078-88.

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